

FIG.1A

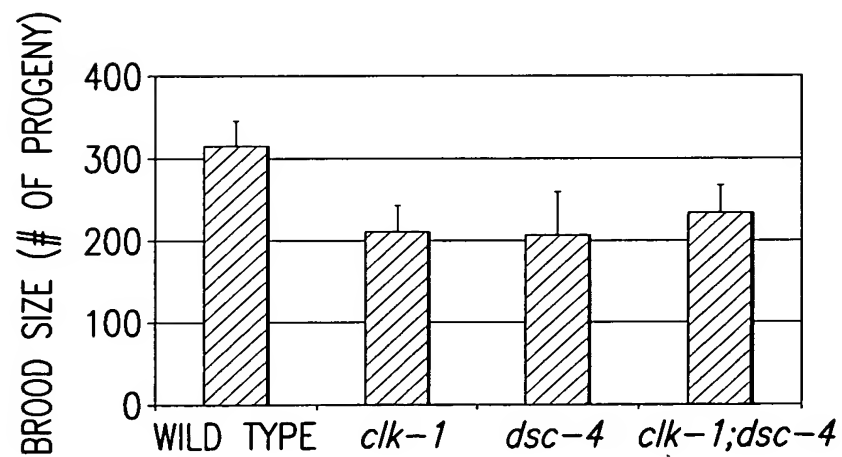


FIG.1B

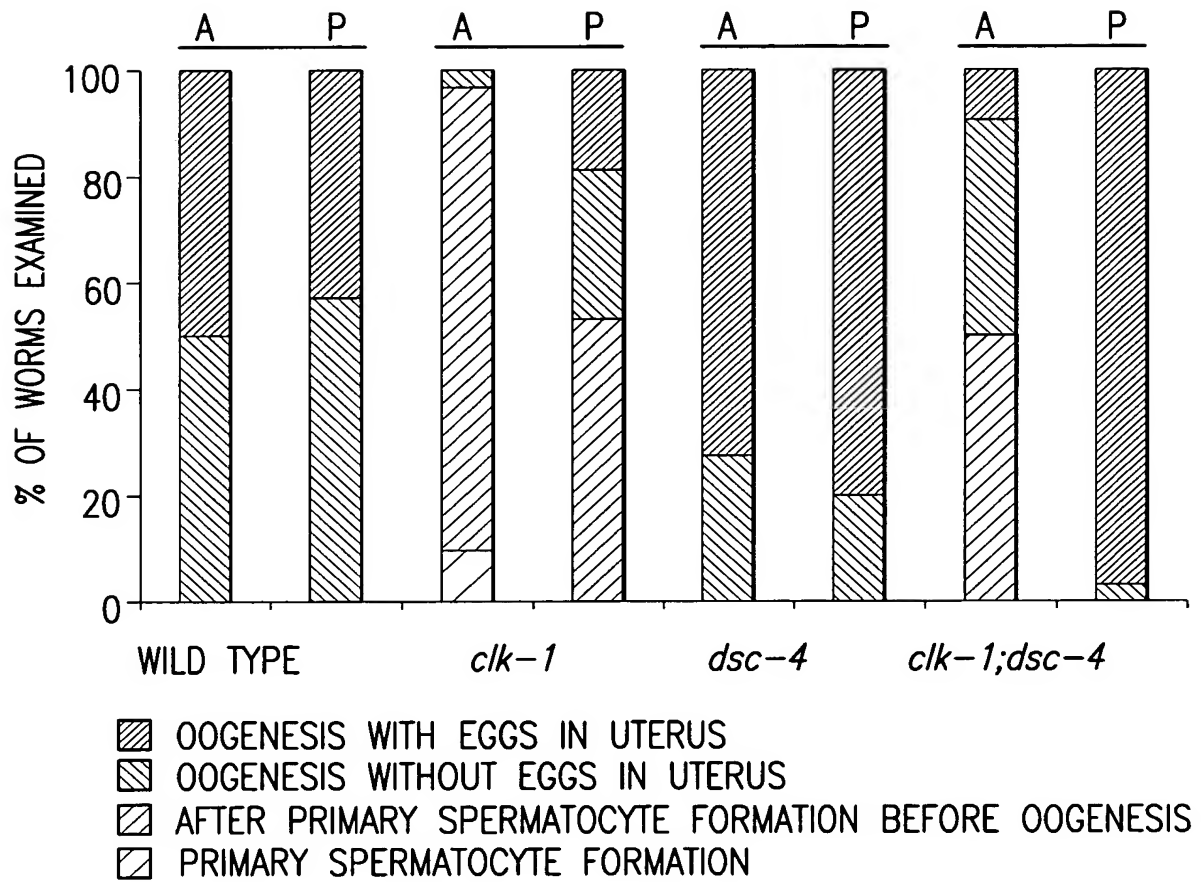


FIG.1C

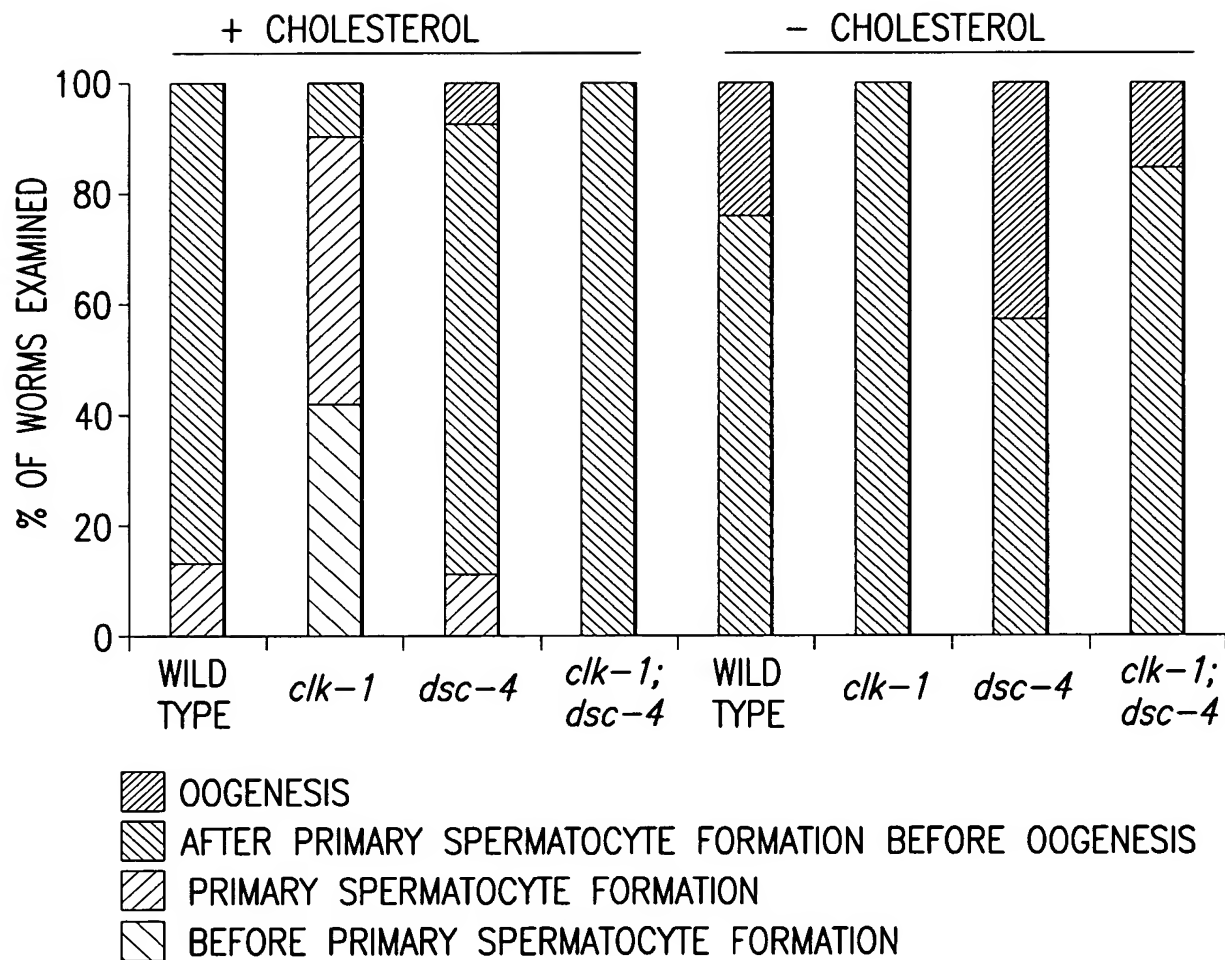


FIG.1D

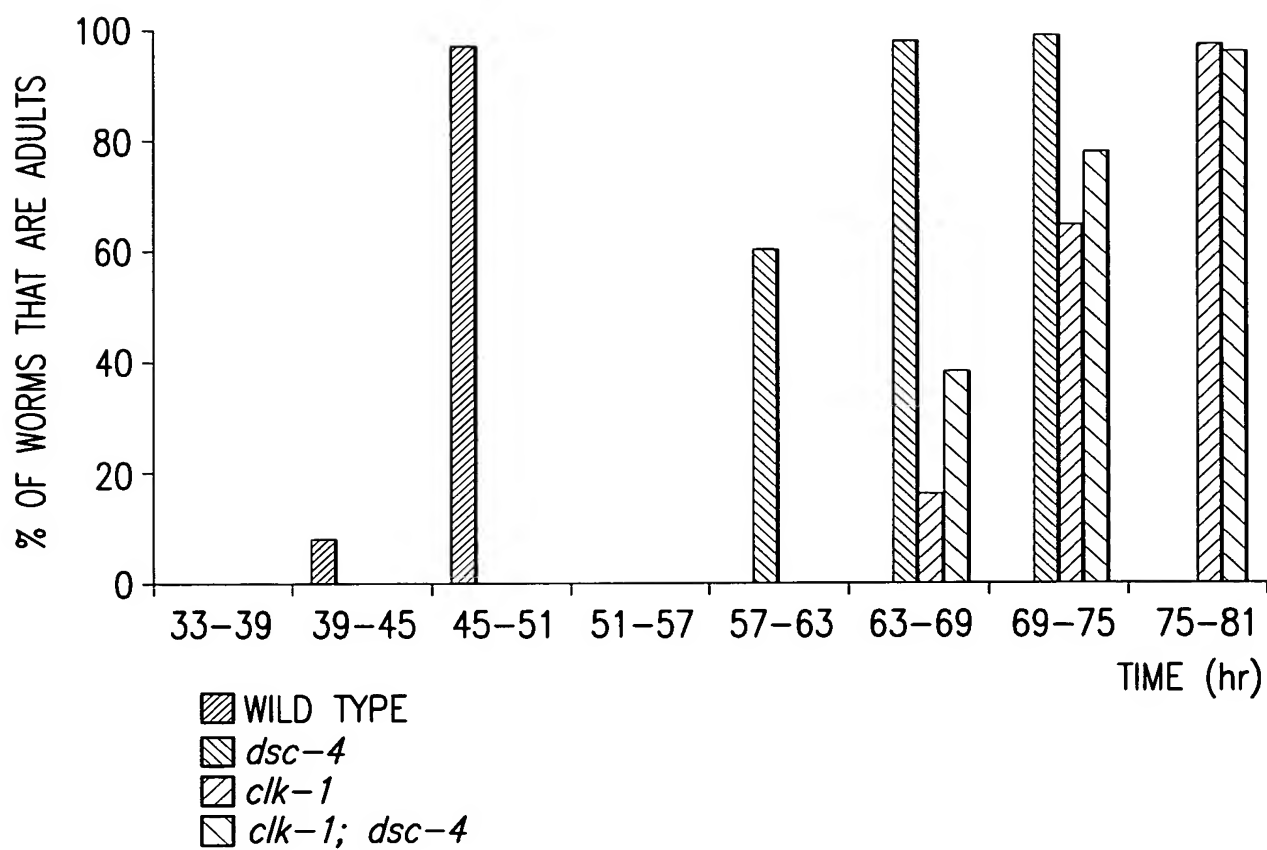


FIG.1E

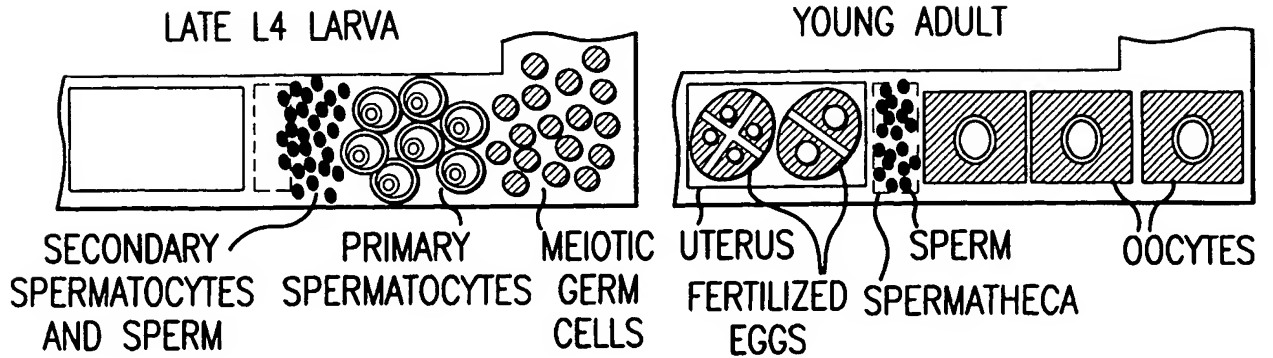


FIG.2A-1

FIG.2A-2

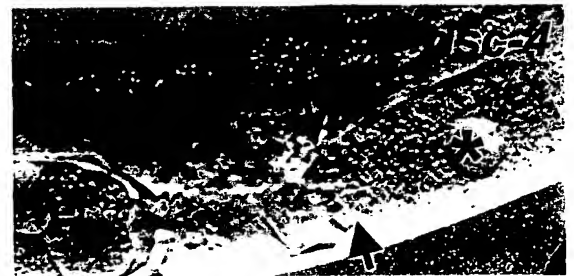


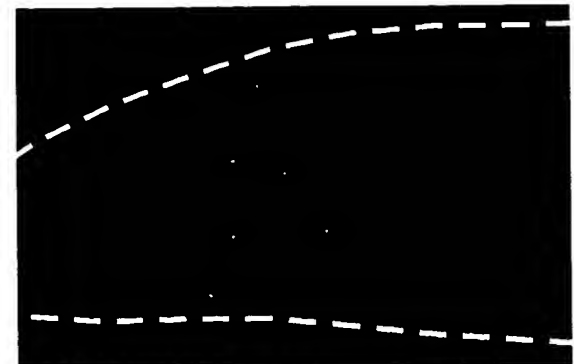
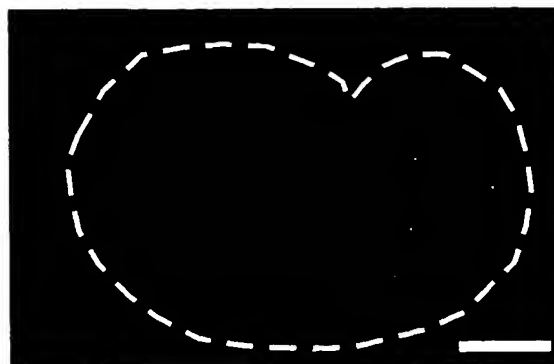
FIG.2B

FIG.2C



FIG.2D

FIG.2E



Dsc-4	AVPDLDEIKKNLRKHGPDYYKNQPKMNEIVRLKVDYWFRTESMIYDDIDNKEKDPSTVIAGNFSFETLHHDVEGMLGRFTLT	85
Zebrafish	.....AGPRLDNGKLYRYSYGFEVGNRP TGSPENGVGR ISSDVD INLAWRNPE IQDEQLLQVQISNIQVESAGKH	72
Mouse	.....VKGHTTGLSLNNRLYKLYSYSEVFEVFDGGKGPQDQSVGYKISSDQVLLWRNP DGGDDQV IQVTITAVNVE NAGQQ	77
Human	.....VKGHTTGLSLNDRLYKLYSYSEVFEVLDRGKGLQDQSVGYRISSNVDAVALLWRNP DGGDDQL IQITMKDQVNVNQQ	77
Dsc-4	QCNTDNCGNPPIYIAFR.....QGGNNAEHLKASDESATWNFLYAIIVTITYTPAEYEGDEQTVDT.....IYGRFYNFGR	160
Zebrafish	SRKNNIFHGSSEAESLCKVRLEALQRPFLVLWKMGKIRSLYAQKAEPATVKKLRGVASMLMMQLKSGKMSEADASCKLVEYKV	157
Mouse	RCEKSIFQKSTPKIIGKDNLEALQRPMLLHLVRGKVKEFYSENEPVGIEKLRGLASLFQMQLSSGTTNEVDISQDCKXYTQA	162
Human	RGEKSIFGKSPSKMGENLEALQRP TLLHLIHGKVKEFYSYQNEAVAIEKLRGLASLFTQLSSGTTNEVDISQDCKXYTQA	162
Dsc-4	PEDKRFERRIEKCDLGYGTNFKFEGIESVQYQDQVWYIQNTKVDADIIMVDATIEMLAFKSPLEHKYGTLESRTHVEITNRTV	245
Zebrafish	NKHQVIRTKHLETKSQETGETHS.PVLGISGKCAAEIVITLENGIIKSADAKETHVLSINARHKAAKVL\$RQSLTLKAIEAG	241
Mouse	QDDKVVKIKALDTCKIERSGFTAN.QVLGVSSKATSVZTYKIEDSFVAVLAEETRAFALNQQT IAGKIV\$KQKLELKTTEAG	246
Human	HQDKVIKIKALDSCKIARSGFTPN.QVLGVSSKATSVZTYKIEDSFVAVLAEETHNFGLNFLTQTIKGI\$KQKLELKTTEAG	246
Dsc-4	FVTSYCNTPVPSAKCAEQAFGAVRVGGKLYEHVKIAEQSNKZTKLIGTYRRHIZQDMGDSHICEKHSLSYSQIAQEARLAKRQDW	330
Zebrafish	PAEVAGKDVAGVVKALDDKFLSVGVIVEKTKPKCKG...CPNMETWKAVERSQEFPNSL\$KAEAPRSFZTLVHSLRKSSKSEILT	323
Mouse	PRMIPGKQVAGVIAVDSKYKAIPIVGVQLERVCKG...CPSAEHWKSI\$KNEPENL\$KAEAVQSFZAF IQHLRTSRREEILQ	328
Human	PRMSGKQAAAIIKAVDSKYTAIPIVGVQVQSHCKG...CPSSELRWRS\$KTYQPDNL\$KAEAVRNFAF IQHLRTAKKEEILQ	328
Dsc-4	EAAIQPENDHVZSLIASALGGVGTAE\$TTAREVLLTASPDYDDLZFCISQSSNN\$KWHKQ\$MYWLGSLDKKSEYWK\$ANT	415
Zebrafish	VLQNSKTAIPQVDAVTSAQTPSSLSA\$LEFLDFSKKDGILQERFZYACGFASHPT\$SMLQS\$LEVSQKIGSTEIKES\$VII	408
Mouse	ILKAEKKEVLPQVDAVTSAQTPDSLEA\$LDFLDFKSDSSIILQERFZYACGFATHPDELLRA\$LSKFKGSFASNDIRES\$MII	413
Human	ILKMNKEVLPQVDAVTSAQTSDSLEA\$LDFLDFKSDSSIILQERFZYACGFASHPN\$ELLRA\$LSKFKGSIGSSDIRET\$MII	413

FIG. 3A-1

Dsc-4	IATVLRGEASTSSNSCNKG <del>ET</del> IVNKFITDLTAGGVEVRV <del>EV</del> LENIPIF <del>SY</del> TFA <del>K</del> FICETESEDVQKAALNVIEAASKN	500
Zebrafish	MGALLRL <del>Q</del> LKGACD <del>P</del> WLVK <del>ELL</del> AGPDSTQE <del>EE</del> SEVQMYL <del>ALK</del> NALLPE <del>Q</del> IPVLTK <del>YAE</del> SEVGA...YSTIAITAK <del>Q</del> RYDP	490
Mouse	IGALVR <del>KL</del> QNEGCK <del>K</del> AVVEA <del>K</del> KLILGGLKPEKKEDTMYL <del>ALK</del> NALLPE <del>Q</del> IPLL <del>KYAE</del> AGECP...VSHLATTV <del>Q</del> RYDV	495
Human	TGTLVR <del>KL</del> QNEGCK <del>K</del> AVVEA <del>K</del> KLILGGLKAEKKEDTRMYL <del>ALK</del> NALLPE <del>Q</del> IPSL <del>LKYAE</del> AGECP...ISHLATTAK <del>Q</del> RYDL	495
Dsc-4	LYE <del>Q</del> LTH <del>KL</del> IKLFRNTCSQETPTSHSQL <del>AD</del> IDILLKCV <del>Q</del> DHQN <del>AT</del> LIERTE <del>NP</del> DDQEKWHYLKAI <del>E</del> ASGNKDELKAEFWSR	585
Zebrafish	ALI <del>AE</del> VK <del>K</del> ALNR <del>IY</del> HQNQR <del>IY</del> EKNVRAA <del>ADV</del> IMSSN <del>PS</del> YME <del>KN</del> LL <del>ES</del> IGH <del>P</del> HEMNKYMLSKI <del>Q</del> DVLR <del>FQ</del> MPAYKLV <del>RQ</del> VMK	575
Mouse	SF <del>I</del> DEVK <del>K</del> TLNR <del>IY</del> HQNRK <del>KV</del> HEKTV <del>RT</del> AAVILKN <del>PSY</del> MD <del>KN</del> IL <del>ES</del> IGEL <del>PK</del> EMNKYMLTVVQDILHFEMPASKMIRRVLK	579
Human	PF <del>I</del> DEVK <del>K</del> TLNR <del>IY</del> HQNRK <del>KV</del> HEKTV <del>RT</del> AAVILNNN <del>PSY</del> MD <del>KN</del> IL <del>ES</del> IGEL <del>PK</del> EMNKYMLAIVQDILRLEMPASKI <del>VRR</del> VLK	580
Dsc-4	MRKFKVFRPNFLH <del>R</del> ALQ <del>AD</del> SHVHWQEIADASN <del>FQ</del> ESTANTEFLQSK <del>F</del> KRS <del>F</del> ELSMKKGRKEHNL <del>F</del> SLSIDT <del>EH</del> LEQFVIGSAS	670
Zebrafish	DMISHNYDRFSK <del>TG</del> SSS <del>AY</del> SGFMAETVDVICTYN <del>ED</del> ILYSGSVLRRSNM <del>N</del> Y <del>YG</del> QSNALLHGLQVTIEAQGL <del>ES</del> PIAATPDEGE	660
Mouse	EMAVHNYDRFSK <del>SG</del> SSS <del>AY</del> TGYVERSPRAASTYS <del>ED</del> ILYSGGILRRSNL <del>N</del> FQYIKGTELHGSQVIEAQGL <del>EG</del> LIAATPDEGE	664
Human	EMVAHNYDRFSR <del>SG</del> SSS <del>AY</del> TGYIERSPRSASTYS <del>ED</del> ILYSGGILRRSNL <del>N</del> FQYICKAGLHGSQVIEAQGL <del>EG</del> ALIAATPDEGE	665
Dsc-4	SRSGAPQ <del>Q</del> SVRIGVAGHK <del>EP</del> THH <del>IF</del> K <del>Q</del> ST <del>DL</del> L <del>ST</del> WMEAD <del>Q</del> ERTHKAF <del>EG</del> HVPVR <del>Q</del> SVPL <del>SL</del> TLDVD <del>SV</del> GAI <del>SMR</del> VLASA <del>EV</del>	755
Zebrafish	EELESFA <del>Q</del> .MSALLFDVQ <del>Q</del> RPVTF <del>EN</del> K <del>Q</del> YS <del>DL</del> M <del>SK</del> MFST <del>SD</del> DPINVK <del>GL</del> ILLT <del>HS</del> QV <del>IP</del> Q <del>SG</del> LRASAEFQAGLSIDISGGM <del>EF</del>	744
Mouse	ENLDSYA <del>Q</del> .MSAILFDVQ <del>Q</del> RPVTF <del>EN</del> K <del>Q</del> YS <del>DL</del> M <del>SK</del> MLSAS <del>SD</del> DPVSVVK <del>GL</del> ILLT <del>HS</del> QD <del>IQ</del> Q <del>SG</del> LKANMEIQGGLAIDISGSM <del>EF</del>	748
Human	ENLDSYA <del>Q</del> .MSAILFDVQ <del>Q</del> RPVTF <del>EN</del> K <del>Q</del> YS <del>DL</del> M <del>SK</del> MLSAS <del>SD</del> DPISVK <del>GL</del> ILLT <del>HS</del> QELQ <del>Q</del> Q <del>SG</del> LKANIEVQGGLAIDISGAM <del>EF</del>	749

FIG.3A-2

Dsc-4  
Zebrafish  
Mouse  
Human

~~SLVWNRQ~~. . . NAKAEAYTSGSLHLZASLYHHSEPVHRVESZISA~~STFT~~TDTRAIFETL~~TPYDF~~CLRTSN~~SNVD~~INQ~~KT~~VVQDQICK 838  
~~SLVWYRES~~KT~~SVNN~~RGALVIIGNM~~VD~~TDFVSAGVEVGFE~~FEAT~~DFIT~~TVQF~~SEYPF~~VCMQMD~~KTTFPFRETVS~~QEK~~LPTGQM 829  
~~SLVWYRES~~KT~~RVKN~~RVAVVITSDV~~VD~~ASFKAGLESRAE~~FEAG~~FEFIS~~TVQF~~SQYPF~~VCMQMD~~KAEAPLRQFET~~KYER~~LSTGRG 833  
~~SLVWYRES~~KT~~RVKN~~RVVT~~VT~~ITDI~~VD~~SSFVKAGLETSTE~~FEAG~~FEFIS~~TVQF~~SQYPF~~VCMQMD~~KDEAPFRQFEK~~KYER~~LSTGRG 834

Dsc-4  
Zebrafish  
Mouse  
Human

HKKKTLNRKRVHP~~Q~~VTYR~~Q~~DDSTIRQ~~Q~~NSYLEQFRL . . . . . 874  
FSRKRS.RDQVVP~~Q~~SEFP~~Q~~HQENS~~M~~KKVFEPAW . . . . . 863  
YVSRRR.KESLVA~~Q~~CELP~~Q~~HQQNSE~~M~~NNVFPQPESDNSGGWF 876  
YVSQKR.KESVLA~~Q~~CEFP~~Q~~HQENSE~~M~~KVVFAPQPD~~S~~.TSSGWF 876

FIG. 3A-3

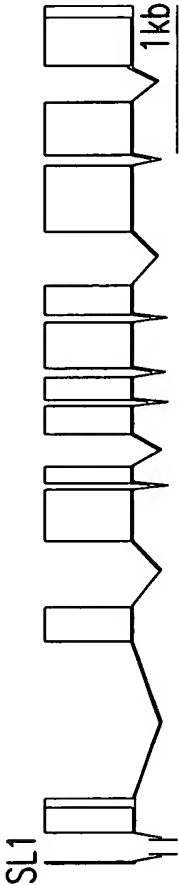


FIG. 3B

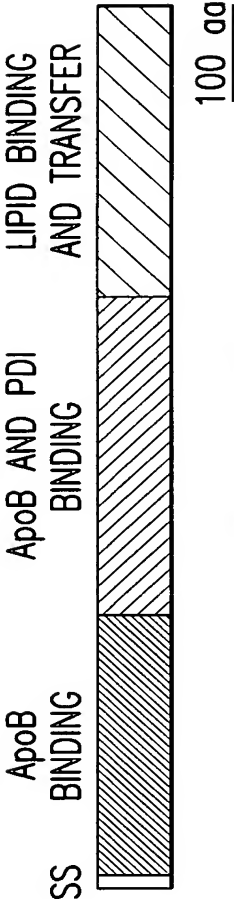


FIG. 3C



1 TTTAATTACCCAAGTTGAGTGTTATCAGCAAGCATAAATCATAACTCTTATCAATAGTACTGCTTCTCTGCAATTCACAAATTCCTCTTCCATCCAAACA

106 G G A C T C C A T T G C C A T A A A A T T A T T T T G C T C T C T G G G A G A A A T T T G G A A C C A G A G A T G T T C T C A T C A C G G A T A T G G C T G C T T C T G G C G T T A C T G T  
 1 M F S S R I W L L L A V T V

211 G G G A G T T T G C C T A G C A G T T C C G G A T C T C G A T G A A A T C A G A G A A C C T T C G C A A C A T G G T C C A G A C T A C T A T A A A A T C A G C C G A A A T G A A C G A G A C A C T G T  
 15 G V C L A V P D L D E I K K N L R K H G P D Y Y K N Q P K M N E N T V

316 C C G A C T A C T G A A A G T G C A T T A C T G G T T C C G T A C T G A A T C T A T G A T T T A C G A T G A T A T T G A T A A T A A G G A G A G G A T C C A T C G A C C G T T A T T G C T G G A A A T T T C A G  
 50 R L L K V D Y W F R T E S M I Y D D I D N K E K D P S T V I A G N F S

421 C T T T G A A A C A C T T C A T C A G C T G G A G G T G C G A T G T T G G A C C G T T A C C C T A A C C C A A T G C A A C A C T G A C A C T G T G G T A A T C C A T C T C C A A T C T A C A T A G C  
 85 F E T L H H D V E G G M L G R F T L T Q C N T D N C G N P S P I Y I A

526 A T T C C G T C A A G G T G G T A A T A T G C G G A G C A T A T C C T T A A A G C G T C C G A T G A G A G T G A C C C A C C T G G A A T T T C C T G T A C G C A A T T G T G A A T A C A A T C T A C A C C C C  
 120 F R Q G G N N A E H I L K A S D E S D A T W N F L Y A I V N T I Y T P

631 A G C A G A T A C G G A A G G A C A G C A A C A G T C G A C A C A A T T T A C G G A A G A T G C T T C G T G A A C T T T G G A A G C C A G A G A T A A A C G G T T T A G A A G A A T T A T C G A  
 155 A E Y G E G D E Q T V D T I Y G R C F V N F G R P E D K R F R I I E

736 G A A G T G T G A T T T G G G T A C G G C A C A A A T T T A C G A A A T T C G A A G A A T C G A G A G T G T T C A A T A T G A T C A G G A T G T C T G G T A C A C A C A G A C A C A A A A G T C G A T G C  
 190 K C D L G Y G T N F T K F E G I E S V Q Y D Q D V W Y T Q N T K V D A

841 A G A C A T T A T T A T G T T G A T G C T A T T A G C A T T C A A G A G T C C A C T T C A C G A G A A A T A C G G A T T C A C T C T G G A A T C C A G A A C T C A C G T A G A A A T C A C C A A  
 225 D I I M V D A I E M L A F K S P L H E K Y G F T L E S R T H V E I T N

FIG. 4A

946 CCGTACACGTGCTTCGTCACCAGCTACTGTAATGATACCGTACCATCGCCAAATGCGCCGAGCAGCGTTTGGAGCAGTTCCGTGTCGGAGGAAACTTTACGA  
260 R T R V F V T S Y C N D T V P S A K C A E Q A F G A V R V G G K L Y E

1051 GCATGTCAAGATTGCCAGGAACAGTCGAATAAGTTAACAAAGCTTATTGGAAACATACCGCGGTCACTCTTCAAGATATGGTGACTCACACATTTGTGAGAAACA  
295 H V K I A Q E Q S N K L T K L I G T Y R R H L Q D M G D S H I C E K H

1156 TTCITTGCTTTATAGTCAAAATTGCTCAAGAAGCCCGATTGGCTAAGCGACAGGACTGGGAAGCTGCTATCCAATACCCAGAGAATGATCAITCTAICITTAI  
330 S L L Y S Q I A Q E A R L A K R Q D W E A A I Q Y P E N D H V L S L I

1261 CGCCAGTCCCTCGGAGGAGTCGGTACAGCAGAACTCTATCACCACITGCTCGTGAAGTTCTTCTTACCGGTCCCGCTGATTATCTTGATGATTTACTTTTGGAAAT  
365 A S A L G G V G T A E S I T T A R E V L L T A S P D Y L D D L L F G I

1366 TTCACAAAGCTCGTCTAACAAATGGCACAACAATTGATGTACITGGCTCGGTCCTTGATATAAAAAATCAGAAGAAATATTGGAAGGTGGCTAACACAAT  
400 S Q S S N N E K W H K Q L M Y W L G S L D K K S E E Y W K V A N T I

1471 TGCAACTGTGCTGAACAACGATGTGAAGCATCGACAAGCAGCTTAAACITCTGCAATAAAGGAAGGAACGATTGTCAACAAATTCATCAGCTGACCIGACAGC  
435 A T V L N K R C E A S T S S L N S C N K G K E T I J V N K F I T D L T A

1576 TGGTGGAGTTGAAGTCAGAGTTCTCGAGGTCTCGGAGAATATCCAAATTTTCGGATCCTACACITTTTGGTAAGAAATTCATATGTGAAGTGTGAGGAGATGT  
470 G G V E V R V L E V L E N I P I F G S Y T F A K K F I C E T E S E D V

1681 TCAGAAAGCCGCACTCAACGTTATTCTGGCTCGGAGCAAGAATTGTATGAACACAACACTCACCCACAAGCTCATCAAACTCTTCGGAACACATGCAGCCAGGA  
505 Q K A A L N V I L A A S K N L Y E T I Q L T H K L I K L F R N T C S Q E

1786 AACTCCAACCTTCATCTCAACTCGCCATCGACATCTCTCTCAAAATGTCCTGATCATCAAAACGTTGGCCACCTTGATCTCTCGGAACCTGAGACTCTTAACCC  
540 T P T S H S Q L A I D I L L K C V P D H Q N V A T I L I L R T E T L N P

FIG.4B

1891	CGATGATCAGCAAAATGGCATTACCTGTACAAAGCCTATCCAGCGCAAGCGAAACAAGGATGAACCTGAAGCCGAAATTTGGTCGCGAATGCCGAAGTTTAAGGT
575	...D D Q E K W H Y L Y K A I E A S G N K D E L K A E F W S R M R K F K V
1996	TTTCCGACCAAACTTCTTGCACAGAGCACTTCAGCGGATTCTCATGTTCACCTGGCAAGAGATTGCAGATGCTTCAAACCTTCCAACCTGTTCTCCACTGCGAACAC
610	F R P N F L H R A L Q A D S H V H W Q E I A D A S N F Q L F S T A N T
2101	AGAATTCTTGCAAAAATCCTTTAAGAGATCCATCTTTGAGCTATCGATGAAGAAGGGAAGGAGGACACAATTTATTCGCTCCTCCATCGACACTGAGCACCT
645	E F L Q K K S F K R S I F E L S M K K G R K E H N L F S L S I D T E H L
2206	TGACCAATTGTGACTGGATCAGCTTCTTCAAGATCCGGCGCTCCACAAAGGTCGTTCGAAATTGGAGTTGCTGGTCACAAGCTACCAACICACCACATCTTCAA
680	E Q F V T G S A S S R S G A P Q G S V R I G V A G H K L P T H H I F K
2311	GGGAAGTACTGACCTGCTTCCACTGTCTGGAAGCAGATGGAAGGACCGCATAGGCATTGAAGGTCATGTTCCTGTAGAGACGTTGACTATCGGTGCCATT
715	G S T D L L S T V W E A D G R T H K A F E G H V P V R D V R L S V P L
2416	GCTCTCTGGATTGACTCTTGACGTTGATAGCGTTGGAGCAATTAGTAGAGAGTTCTTGCAATCGCGGGAAGTTTCCCTTTGGAATCAGAGATCGAATCGAAAGGC
750	L S G L T L D V D S V G A I S M R V L A S A E V S L W N Q R S N A K A

FIG.4C

2521 AGAGGCATATACATCGGATCCTTACACCTAACGGCTTCCCTCTACCATCACTCAGAACCCAGTCGCCACGTGGAATCCACAACTCTCGGGCTCTCCACCTTCAC  
785 E A Y T S G S L H L T A S L Y H H S E P V R H V E S T I S A L S T F T

2626 CACAGACACCCGTGCAATTTTCGAGACTCTCCCATATGACTTCGCTAGCAACATCTAATAGCAATGTTGATATCAATCAGAAAACAGTTGTACAGGATCAAAAT  
820 T D T R A I F E T L P Y D F C L R T S N S N V D I N Q K T V V Q D Q I

2731 TCGAAAGCATAAAAGAGACGCTTAATCGAAAACGAGTACATCCCTGGAGTTACATACAGGTTGGATGACTCGACGATTCGGCAGTGTAAATAGTTATTGGAGCA  
855 G K H K K K T L N R K R V H P G V T Y R L D D S T I R Q C N S Y L E Q

2836 GTTTAGATTGTAGTTGTTGTTTTTTTTTATTACATTTCATGTTTCTCGGAATCAAAATAAAAAATAACTTATTGAGAAAAAAA  
890 F R L \*

FIG. 4D

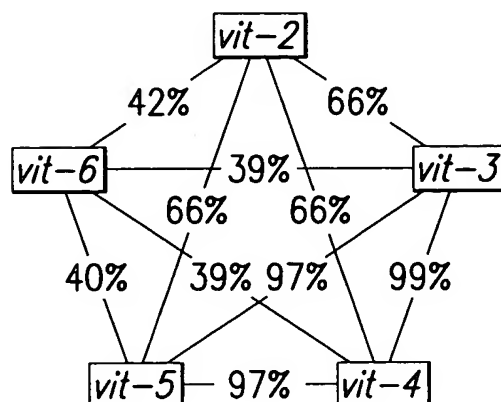


FIG.5A

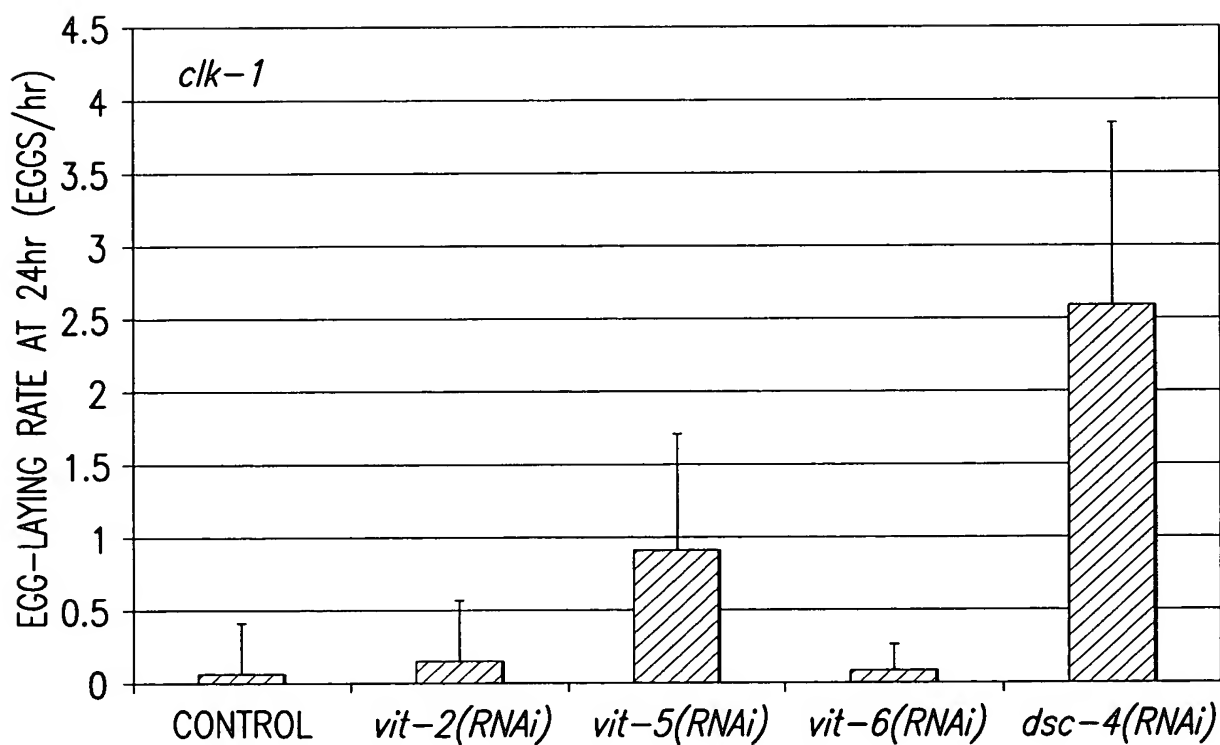


FIG.5B

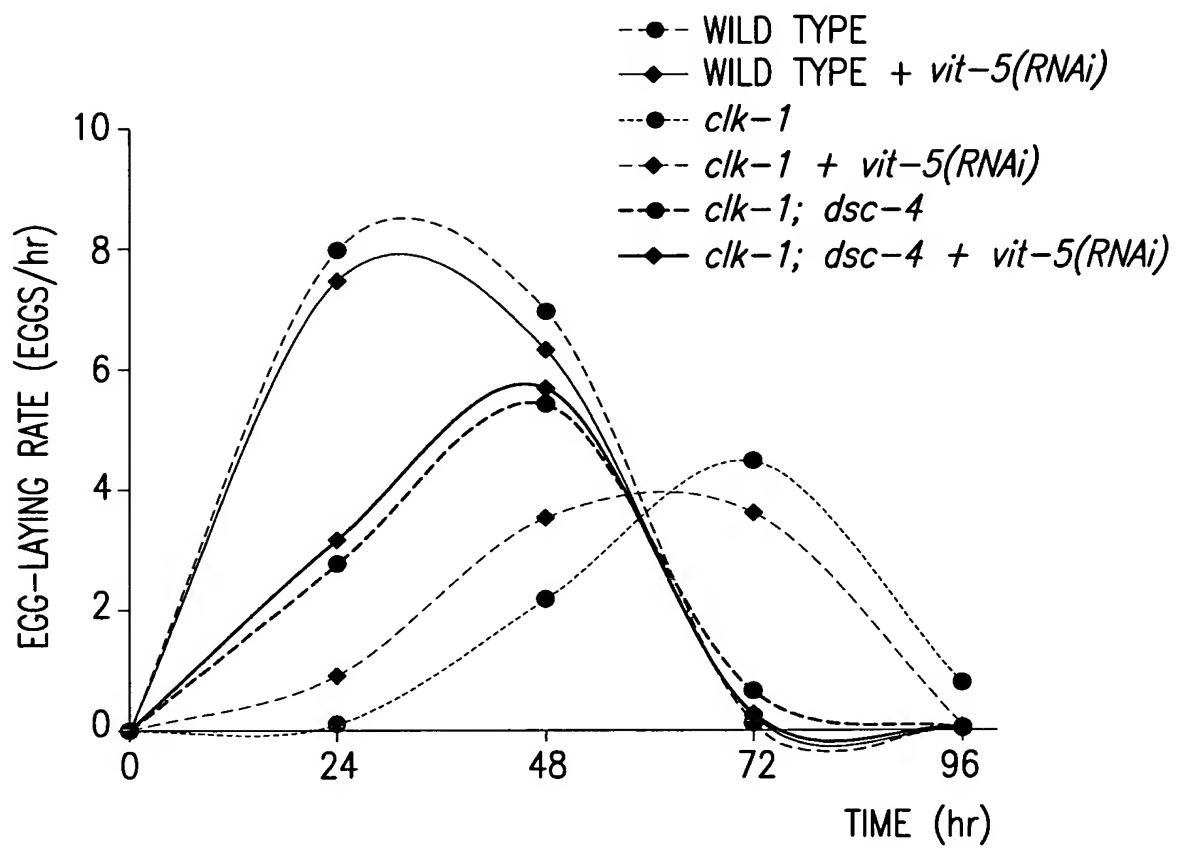


FIG.5C

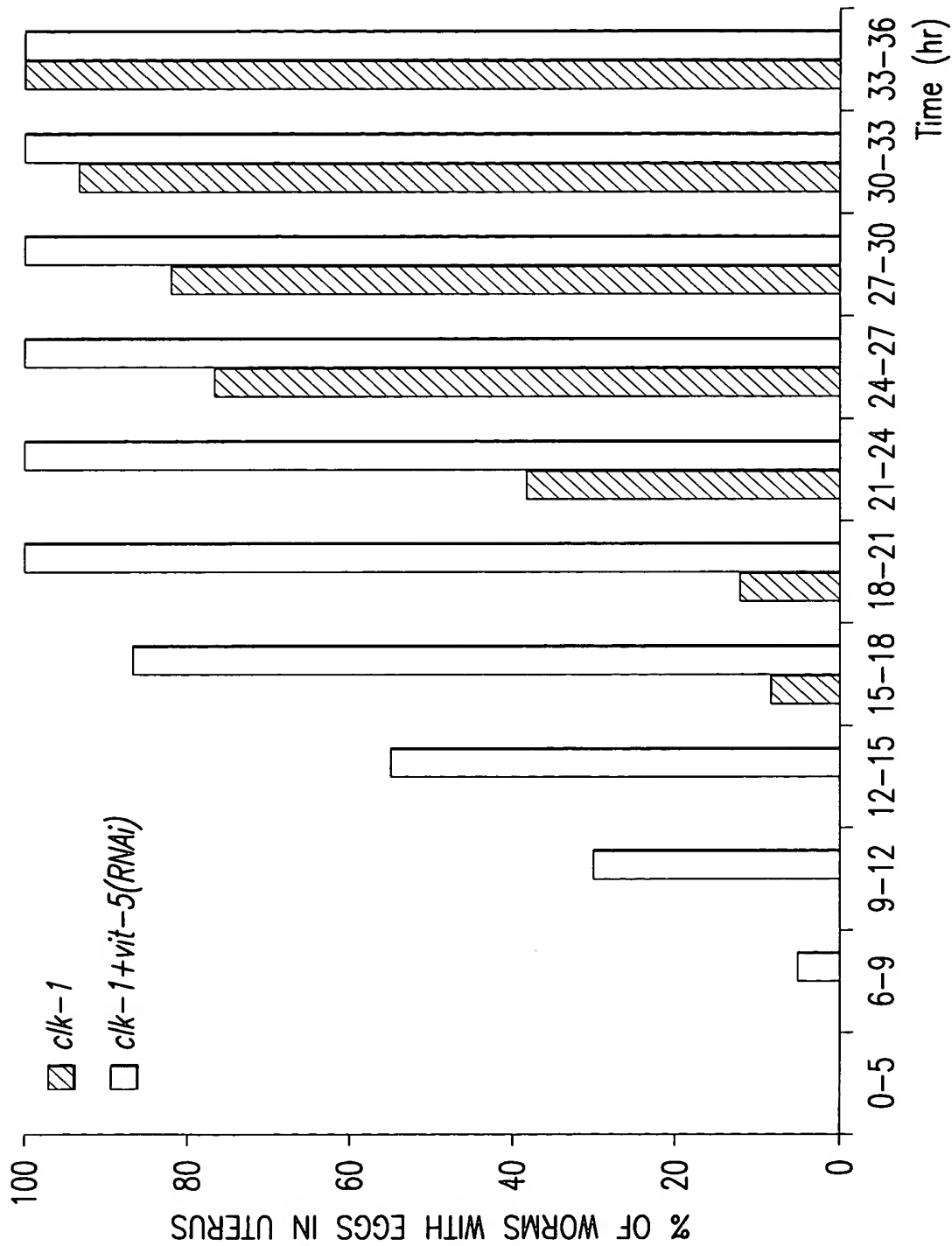


FIG.5D

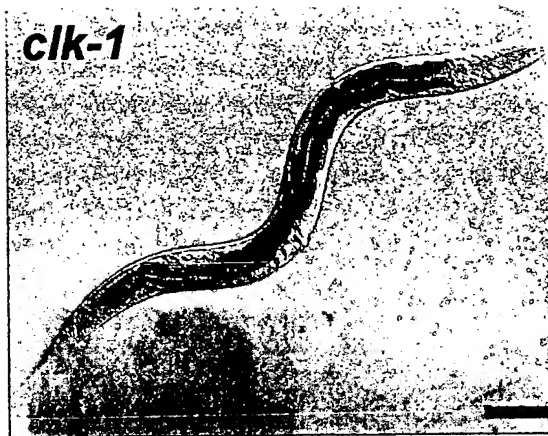


FIG.5E

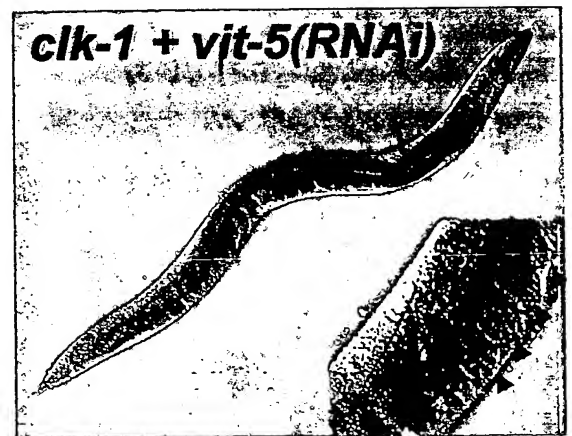


FIG.5F



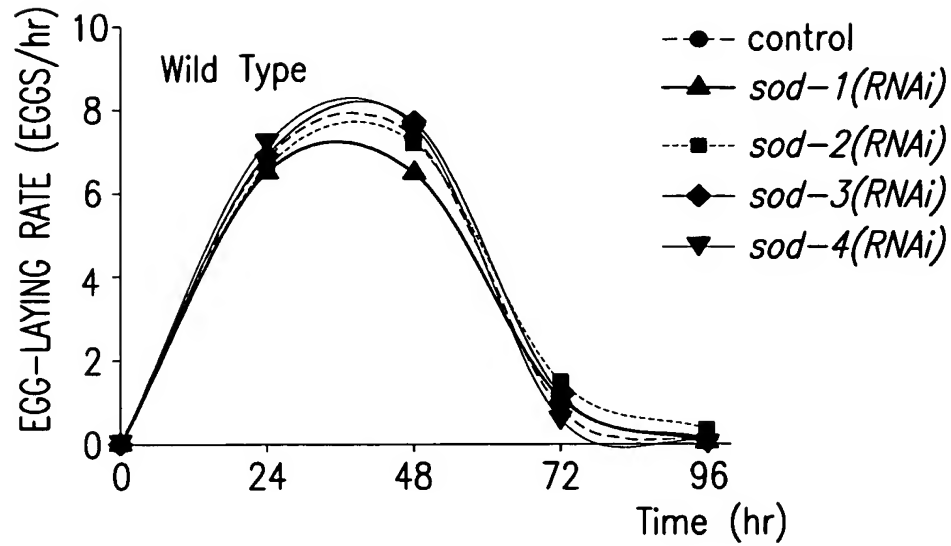


FIG.6A

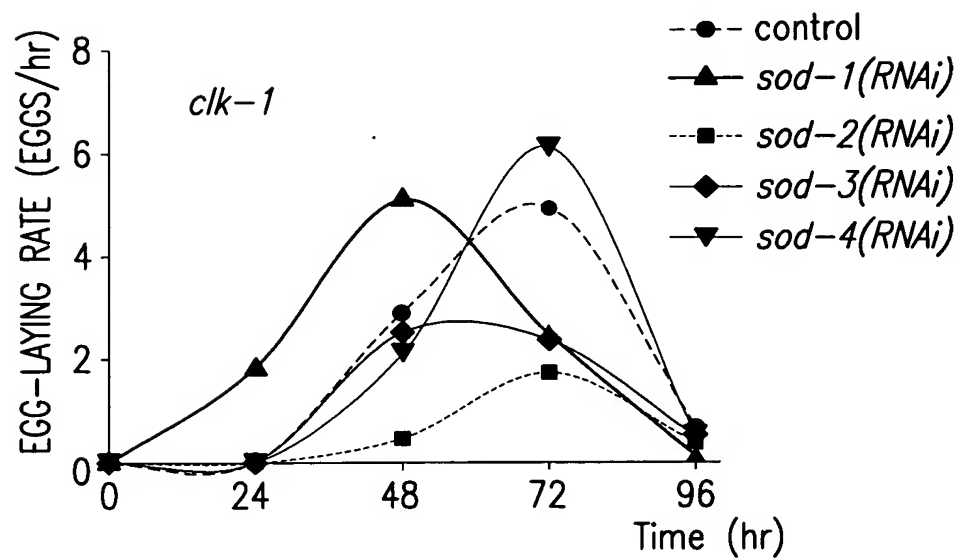


FIG.6B

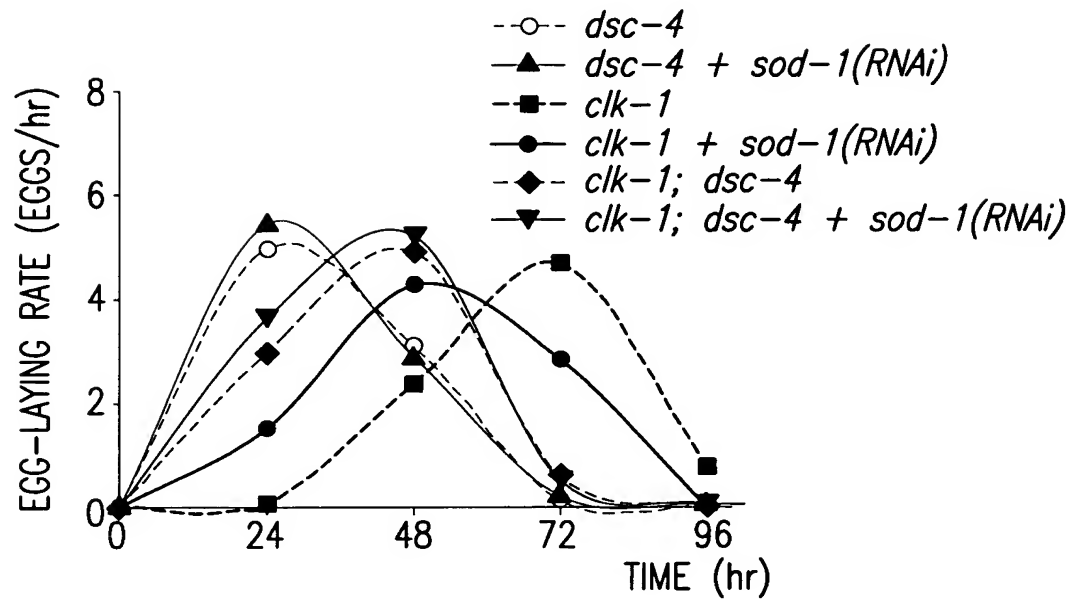


FIG.6C

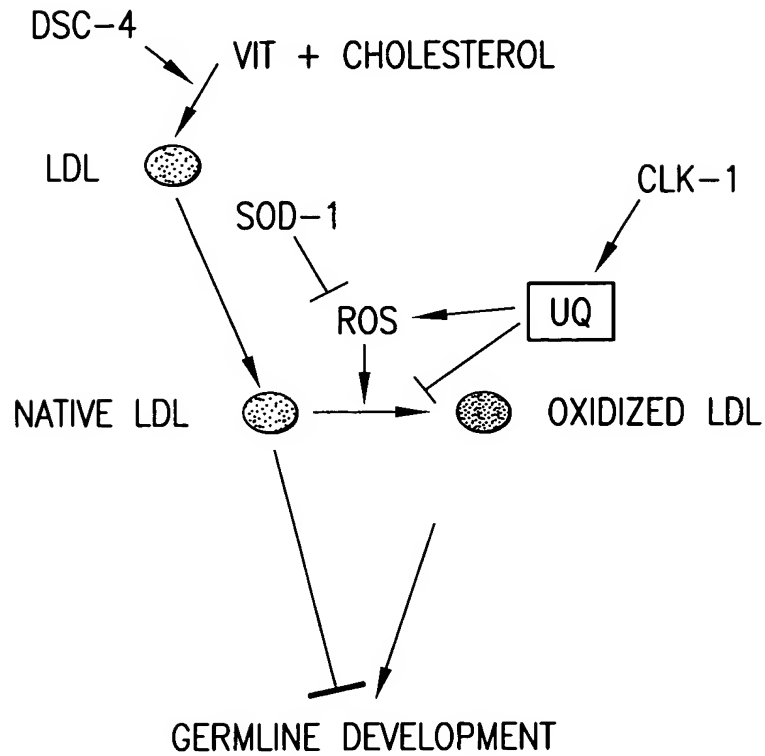


FIG.7A

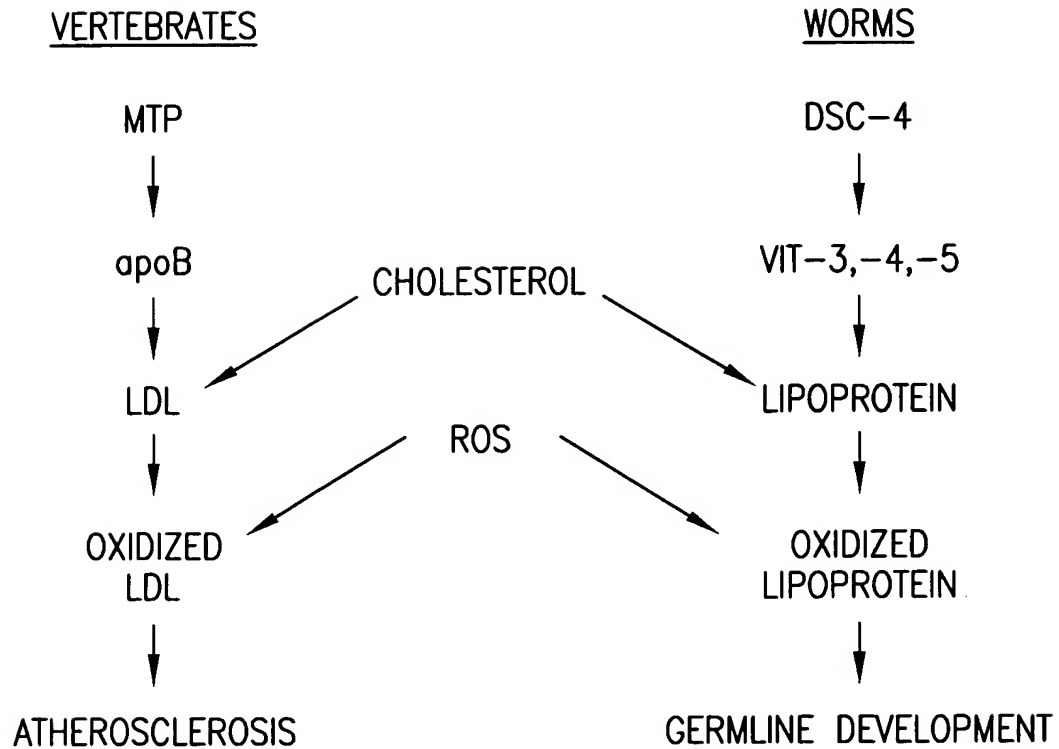


FIG.7B

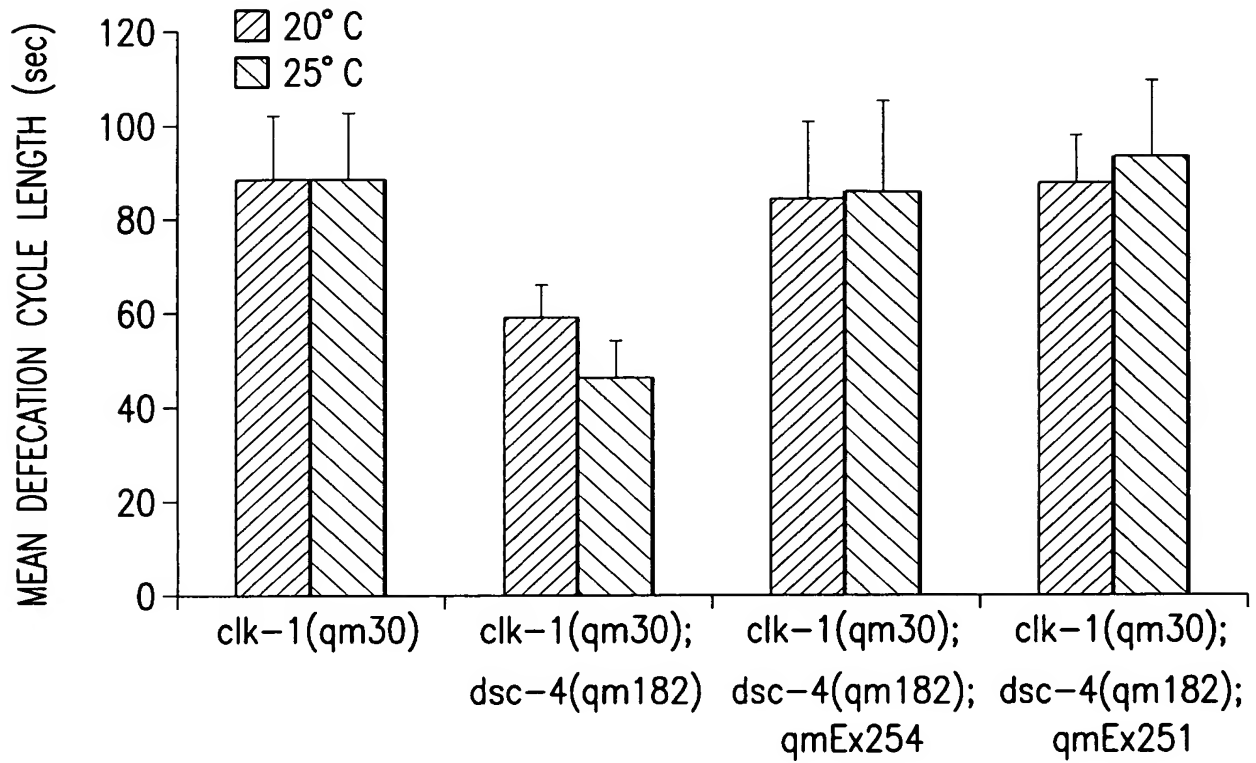


FIG.8A

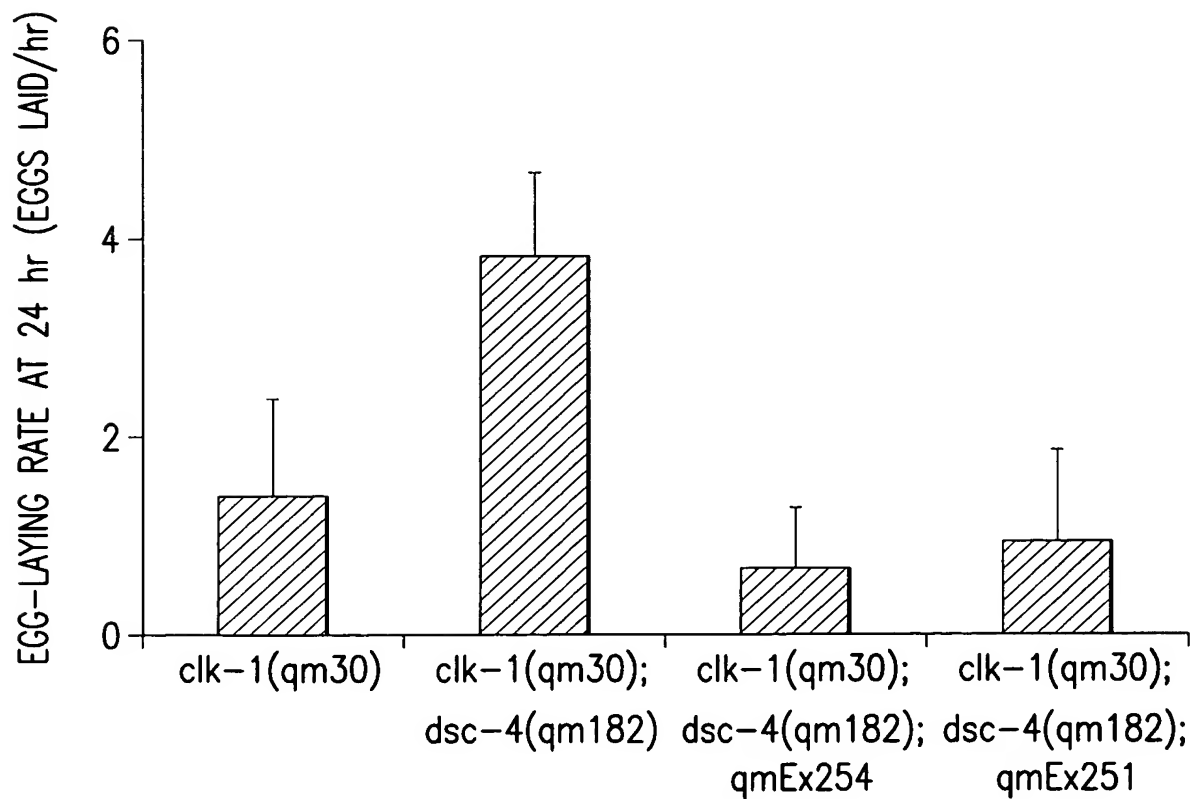


FIG.8B

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1      ATGTTCAAGT GGTGCCATG CTGTTCAAGT ACTTCAAACG AAAAGAATGC GCCGACGGAA
61     CGAAGATTAC GAGCTAACGA TAGGGAATAT AATGCACAAT TCAAATATGC AGACAATGTA
121    ATCAAAACGT CCAAATACAA TATAATCACC TTCATTCTC AAAATTTATT CGAACAATTC
181    CAGCGGATAG CCAACTTTTA TTTTCTAGT TTAATGATAT TACAGTTTAT TCCTCAAATT
241    TCCTCAATTT CCTGGTATTC TACAGCGGTT CCACTGGTTA TTGTATTGGC ATTTTCAGCT
301    ATTAAAGATG GGTACGATGA TGCACAAAGG CACATATCTG ATCGAAATGT AAATGGTCGA
361    AAATCCTACG TAGTTCGAAA TGAAGTCTA TGTGAAGAAG ACTGGAGTAA TGTTAAAGTT
421    GGAGATGTGA TACGAATGAT GAGTAATCAA TTTGTGGCGG CTGATCTTCT ATTATTATCA
481    ACGTCGGAAC CATATGGAGT ATGTTTTATT GAAACTATGG AATTGGATGG AGAAACAAAT
541    CTGAAAAATC GTGCCGCTAT TGCATGTACC CAGGAAATGG GCGACGATTT GGATGGGATT
601    ACGCGCTTTG ATGGAGAAAT AATCTGTGAA CCTCCCAATA ACAACTAGA CAAGTTCAAT
661    GGAAAAATTA TATGAATAA TCATGAATAT GGAGTTAATA ATGATAATAT TCTGCTGAGA
721    GGATGTATTT TGAAGAACAC GAGATGGTGT TATGGAGTTG TCGTTTTTGC TGGAAAAGAT
781    ACAAATTAAT TGATGAACAG TGGAAAAACA AAGTTCAAAA GAACGTCTCT CGACCGATTT
841    TTGAATATTT TAATCGTCGG AATTGTGCTT TTTCTCATTG CAATGTGCCT AATTGTGACG
901    ATTTGTGTG CTGTATGGGA ATATCAAAC TGAAGATATT TTAATTTTA TCTACCGTGG
961    GACGATGTGG TTCCTAGTCC TGAACAAAGA GGTGGCCGCC AAATTGCCCT TATCGCCTTC
1021   CTCCAGTTCT TCTCTACAT CATTCTTCTC AATACAGTTG TACCAATTTT TTTATATGTG
1081   TCTGTGGAAT TTATTCGATT TATTCATTCA TTATGGATTA ATTACGACAC TCAAATGTAT
1141   TATGAAATG GAGAGAAAAG TGTCCACGCA AAGGCACATA CAACAACCTT AAATGAGGAG
1201   TTGGGACAAG TTCAATATGT GTTCAGTGAC AAGACTGGAA CGTTGACAAG GAATATTATG
1261   ACTTTTAATA AGTGTACCAT TAATGGGATC TCGTACGGAG ACATTTATGA TCACAAGGGA
1321   GAGGTTATTG AGACGAATGA CAAAACCAA TCTCTCGACT TTTCTGGAA TTCAGCGTCC
1381   GAACCCACAT TCAAATTTT CGATAAAAT CTAGTTGATG CTACAAAACG TCAAGTACCA
1441   GAAATTGATC AATTCTGGAG ACTACTGGCT CTTTGTCTA CTGTAATGCC TGAAAGAGAT
1501   AAAGGACAAC TGGTTTATCA GGCACAATCA CCTGATGAAC ATGCTCTAAC GTCAGCTGCA
1561   AGGAATTTTG GTTATGTTTT CCGAGCAAGA ACGCCTCAA GCATTACGAT TGAAGTGATG
1621   GGAAATGAGG AAATCATGA ATTATTGGCA ATTCTTGATT TTAATAATGA TCGAAAAAGA
1681   ATGCTGTAA TTGTGAAAG ACCTGATGGA AAGATTCGAT TGTATTGTAA AGGCGCTGAT
1741   ATGATGATTA TGCAGAGAAT ACATCCATCA ACATCTCAA TAATGCGTAC CTCAACCAAT
1801   ACTCATCTCG CTGATTTTGC AAATATCGGT CTTGGAACGC TTTGTTTGGG ATACAAGGAT
1861   CTTGATCCAG CGTACTTTTC GGATTGGGAT TCTCGAGTCA AAAAGGCGTC CGCAGCCATG
1921   CAGGACAGAG AATCTGCGGT CGATGCTCTT TACGAAGAAA TTGAAAAAGA TCTGATATTG
1981   ATTGGTGCAA CGGCTATTGA AGACAAGCTT CAGGATGGTG TTCCAGAGGC AATTGCAAGA
2041   CTTTCAGAAG CTAATATCAA GATTGGGTG CTTACCGGGG ATAAGACAGA AACGGCTATA
2101   AACATTGCCT ACTCGTGTG CCTTCTGACC GATGAAACCA AGGAAATTGT TGATGTTGAT
2161   GGGCAAACG ATACCGAAGT CGAAGTACAG CTAAGAGATA CAAGAAACAC ATTTGAACAG
2221   ATTTTGGCAT TGCCGTCACC GCTTGGAGGA AAGCCACGTA TTGAAATTGA GACAATCCAC
2281   GAGGAGTCG AGGCTATTTT CTCTGCAAGG AGTATGGATA GAAACATTGT AACTCCTGAT
2341   TTGAAATCAG CAGAAATGGC TGAACACGAG AGTGGAGGTG TTGCTTTGGT AATAAATGGA

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FIG.9A

2401 GATTCATTGG CTTTGGCTCT TGGTCCAAGA CTTGAAAGAA CTTTCTTGA AGTGGCTTGT  
 2461 ATGTGTAATG CAGTAATATG TTGCGAGTG ACACCACTTC AAAAAGCTCA AGTAGTTGAT  
 2521 CTAGTAAAC GAAACAAAA AGCAGTGACA CTTTCAATTG GAGACGGAGC AAATGATGTC  
 2581 AGTATGATCA AGACAGCTCA TATTGGAGTT GGAATTTCTG GCCAAGAAGG AATGCAAGCA  
 2641 GTATTAGCAT CAGACTATTC AATCGGACAA TTCAAATATC TTGAACGTCT TCTTCTTGT  
 2701 CACGGTCGAT GGTCTTACAT TCGAATGGCA AAGTTCCTCA GATACTTTT TTACAAAAAC  
 2761 TTTGCATTTA CACTTACCA CTTCTGGTAT TCATTCTTCT GTGGATATTC TGCTCAAACA  
 2821 GTTTTTGACG CTGTATTGAT TGCTTGTTAC AATCTCTTT TCACAGCACT TCCTGTTTTG  
 2881 GCAATGGGAT CTTTGGATCA AGATGTTGAT GATCATTATT CACTGAGATA TCCTAAGCTT  
 2941 TATCTGCCGG GACAGTTCAA TTTGTTCTT AATATGAGAA TATTTATTTA TTCTGTACTT  
 3001 CATGGAATGT TTAGTTCCT TGTGATATTC TTCATTCCAT ATGGTGCATT TTACAACGCA  
 3061 GCTGCTGCTT CTGGAAGGA TTTGGACGAT TACTCGGCTC TTGCTTTCAC TACTTTTACT  
 3121 GCATTAGTTG TAGTTGTTAC TGGACAGATA GCCTTCGACA CGAGTTATTG GACGGCAATT  
 3181 TCGCATTTTG TAATCTGGGG ATCACTTGTT CTGTATTCC TTGTTTGCTT CCTTCTTAC  
 3241 GAATGGCTTC CAGTTTCATG GATTGTCAA ACATCATCTT CAATCTCATA TGGTGTGCT  
 3301 TTTGAACAA TGGTTACTCC TCACTTCTGG TTTTCAATTC TAATGGTTTC AGTTGTACTG  
 3361 TTACTACCAG TTATGCTTAA TCGATTCTTC TGGCTTGATA CACATCCATC ATTTGCTGAT  
 3421 AGGCTGAGAA TTGAAAGAA AATGGGCAAG AAACCATCGG CGAAAGATGA TAAAAAACC  
 3481 GCATTCAAAC GCACGGCAGC AACTCGACGA AGTGTCCTG GATCACTTAG AAGTGGTTAC  
 3541 GCATTCTCTC ATTCACAAGG ATTCGGAGAA CTCATTCTCA AAGGAAAATT GTTCAAAAT  
 3601 GTGGAATATC TACGGGGAAA GAATAATTG AATGCGAAAA TTCACCCGAC TTCTGATGAC  
 3661 TTGCAGCCGA TGCTTATTC TAGTGTGCTT GATGACAGCC AAGGAGCTTC AAGTATTAAT  
 3721 GCAATGCACC TTCCAATGGG TACAGTCCA CAGAATGTAC CCCATACATT GAATGTAAAT  
 3781 ACTGATGACT GGTCTCAATC ATCGGATTTT CGTCCAGCCT ATGCAAAGGA ACCATCACCA  
 3841 CTGCAGGGTA CAGTAATCCG TGGCGATGGA CGGAGCCATA GAAACCACGT GTATTCGCGG  
 3901 GAAACTCAGG TGAAGAACA ACCAGACGTA ATCACTCGCC TTAA

**FIG.9B**

1 MFSWLPCCS TSNEKNAPTE RRLRANDREY NAQKYADNV IKTSKYNIIT FIPQNLFEQF  
61 QRIANFYFLV LMILQFIPQI SSISWYSTAV PLVIVLAFSA IKDGYDDAQR HISDRNVNGR  
121 KSYVVRNGSL CEEDWSNVKV GDVIRMSNQ FVAADLLLS TSEPYGVCFI ETMELDGETN  
181 LKNRAAIACI QEMGDDLDGI TRFDGEIICE PPNNKLDKFN GKLIWNHEY GVNDNILLR  
241 GCILKNTRWC YGVVVFAGKD TKLMMNSGKT KFKRTSLDRF LNILIVGIVL FLIAMCLICT  
301 ILCVWEYQT GRYFTIYLPW DDVPSPEQR GGRQIALIAF LQFFSYIILL NTWPISLYV  
361 SVEIIRFIHS LWINYDTQMY YENGEKSVPA KAHTTILNEE LGQVQVFSK KTGTLIRNIM  
421 TFNKCTINGI SYGDIYDHKG EVIETNDKTK SLDFSWMNSAS EPTFKFFDKN LVDATKRQVP  
481 EIDQFWRLA LCHTVMPERD KGQLVYQAQS PDEHALTSAA RNFGYVFRAR TPQSITIEVM  
541 GNEETHELLA ILDFNNDRKR MSVIVKGPDG KIRLYCKGAD MMIMQRIHPS TSQIMRTSTN  
601 THLADFANIG LRTLCLGYKD LDPAYFSDWD SRVKKASAAM QDRESAVDAL YEEIEKDLIL  
661 IGATAIEDKL QDGVPEAIAR LSEANIKIYW LTGDKTETAI NIAYSCRLLT DETKEIVVVD  
721 GQDTEVEVQ LKDRNTFEQ ILALPSPLGG KPRIEIEIHH EESEATSSAR SMDRNIVTPD  
781 LKSAEMAEHE SGGVALVING DSLAFALGPR LERTFLEVAC MCNAVICCRV TPLQKAQVVD  
841 LVKRNNKAVT LSIGDGANDV SMIKTAHIGV GISGQEGMQA VLASDYSIGQ FKYLERLLLV  
901 HGRWSYIRMA KFLRYFFYKN FAFTLTNFWY SFFCGYSAQT VFDAVLIACY NLFFTALPVL  
961 AMGSLDQDQD DHYSLRYPKL YLPGQFNLF NMRIFIYSVL HGMFSSLVIF FIPYGAFYNA  
1021 AAASGKDLD YSALAFITFT ALVVVVTGQI AFDTSYWTAI SHFVIWGSVL LYFLVCFLY  
1081 EWLPVSWIVK TSSISYGVA FRTMVTPHFW FSILMVSVL LLPVMLNRFF WLDTHPSFAD  
1141 RLRIRKKMGK KPSAKDDKKT AFKRTAATR SVRGLRSYG AFSHSQGFE LILKGKLFKN  
1201 VENLRGKNNS NAKIHPTSD LQPMLISSVP DDSQGASSIN AMHLPMTGTRP QNVPHTLNVN  
1261 TDDWSQSSDF RPAYAKEPSP LQGTVIRGDC RSHRNHVYSR ETQVEEQPDV ITRL\*

FIG. 10

H06H21.10a	.....	0
ATP8B1	.....	0
ATP8B2	.....	0
ATP8B3	MGHHPAASSASRTVGGVPSVWSWALCTELASLSALPRDRDCTQMDRWHRANGSTTSAALDARGLPPASPAPTP	75
ATP8B4	.....	0
Consensus		
H06H21.10a	.....	0
ATP8B1	.....	0
ATP8B2	.....	0
ATP8B3	RSTRACPEPSPAPPGDTCGSDVTQECGCPAGIRGVEKIPGSSDDVRLPPSPPEFAAQPGVSGCPRQDTQPM	150
ATP8B4	.....	0
Consensus		
H06H21.10a	.....MFSWLPCCSSTSNEKNAPT	19
ATP8B1	MSTERDSETTFDEDSQPNDDEVVPYSDDETEDELDDQGSAVEPEQNRVNREAEENREPFKECTWQVKANDRKYHE	75
ATP8B2	.....MDTLRAVPLFSISGLFSFPYRVSHG IAGILLGEMAVCAKKRPPEE	45
ATP8B3	AGHSEPGGEAADDECGSPTSMGSLGQREDLQDEDRNSAF.....TWKVQANNRAYNG	199
ATP8B4	.....	0
Consensus		
H06H21.10a	ERRLRANDREYNAQFKYADNVIKTSKYNIIITFIPQNLFEQFQRIANFYFLVLMILQFIPQISSISWYSTAVPLVI	94
ATP8B1	QPHFMNTKFLCIKESKYANNAIKTYKYNATFIPMNLFEQFKRAANLYFLALLILQAVPQISTLAWYTTLLVPLLLV	75
ATP8B2	ERRARANDREYNEKFQYASNCIKTSKYNILTFLPVNLFEQFQEVANTYFLFLLILQLIPQISSLSWFTTIVPLVL	120
ATP8B3	QFKEKVI..LCWQRKKYKTNVIRTAKNFYSFPLNLVEQFHRVSNLFFLIIILQSIPDISILPWFSLSTPMVC	274
ATP8B4	.....	0
Consensus		

FIG. 11A



H06H21.10a	VLAFAIKDGYDDAQRHISDRNVNCRKSYVVRNGSLCEEDWSNVK <del>V</del> Q <del>V</del> IRMMSNQF <del>V</del> A <del>Q</del> L <del>L</del> LLSTSE <del>P</del> YGVQ <del>F</del>	169
ATP8B1	VLGVTAIKDLVDDVARHKMDKEINNRTCEVIKDGRFKVAKWKEIQ <del>Q</del> Q <del>Q</del> IVRLKKND <del>F</del> PA <del>Q</del> IL <del>L</del> SSSE <del>P</del> NSL <del>E</del> Y	225
ATP8B2	VLTIITAVKDATDDYFRHKSDNQVNNRQSQVLINGILQQEQ <del>W</del> MMNV <del>C</del> Q <del>Q</del> IKLENNQF <del>V</del> A <del>Q</del> L <del>L</del> SSSE <del>P</del> PHGL <del>E</del> Y	194
ATP8B3	LLFIRATRDLVDDMGRHKSDRAINNRPQCILMGKSKQKKWQDLC <del>Q</del> Q <del>Q</del> VVCLRKQDNIP <del>Q</del> Q <del>Q</del> MLL <del>L</del> ASTE <del>P</del> SSL <del>E</del> Y	349
ATP8B4	.....MN <del>V</del> K <del>Y</del> Q <del>Q</del> IKLENNQF <del>V</del> A <del>Q</del> L <del>L</del> SSSE <del>P</del> PHGL <del>E</del> Y	34
Consensus	vgd v ad lll ep c	
H06H21.10a	IE <del>T</del> MEID <del>Q</del> E <del>T</del> NL <del>K</del> NRAAIACIQEMGDDLDGITRE <del>D</del> GEI <del>Q</del> Q <del>P</del> PN <del>K</del> LDK <del>N</del> Q <del>K</del> IWNINHEYGVNNDNI <del>L</del> LR <del>Q</del> Q <del>L</del>	244
ATP8B1	VE <del>T</del> AELD <del>Q</del> E <del>T</del> NL <del>K</del> FKMSLEI <del>Q</del> QYLOREDITAT <del>D</del> Q <del>F</del> IE <del>Q</del> Q <del>E</del> PN <del>R</del> LDK <del>E</del> T <del>Q</del> T <del>F</del> WRNTSFPLDADKIL <del>L</del> LR <del>Q</del> Q <del>V</del> I	300
ATP8B2	IT <del>T</del> AELD <del>Q</del> E <del>T</del> NL <del>K</del> VRQAIPV <del>T</del> SELGDISKLAK <del>E</del> D <del>Q</del> EVIE <del>Q</del> Q <del>P</del> PN <del>K</del> LDK <del>E</del> SG <del>T</del> E <del>Y</del> WKENKFPLSNQNML <del>L</del> LR <del>Q</del> Q <del>V</del> L	269
ATP8B3	VE <del>T</del> VIDI <del>Q</del> Q <del>E</del> TL <del>K</del> FRQALMV <del>T</del> HKELATIKKMA <del>S</del> Q <del>Q</del> TV <del>T</del> Q <del>E</del> AP <del>S</del> RMH <del>H</del> FV <del>Q</del> Q <del>E</del> WNDKKYSLDIGNLL <del>L</del> LR <del>Q</del> Q <del>R</del> I	424
ATP8B4	VE <del>T</del> AELD <del>Q</del> E <del>T</del> NL <del>K</del> VRHALSV <del>T</del> SELGADISRLAG <del>D</del> Q <del>E</del> IV <del>Q</del> Q <del>E</del> V <del>P</del> PN <del>K</del> LDK <del>E</del> SG <del>T</del> E <del>Y</del> SWKDSKHSLNNEKI <del>L</del> LR <del>Q</del> Q <del>L</del>	109
Consensus	et dgetn k t f g ce pn f g l w lrgc	
H06H21.10a	K <del>N</del> T <del>R</del> W <del>Q</del> Y <del>G</del> V <del>V</del> VFAG <del>K</del> Q <del>T</del> KL <del>M</del> MS <del>S</del> CKTK <del>F</del> K <del>R</del> TS <del>L</del> DRFL <del>K</del> ILIVG <del>V</del> VLFIAMCLICTILCAV <del>W</del> EYQ <del>T</del> GRYFTI <del>Y</del> LP	319
ATP8B1	R <del>N</del> T <del>D</del> E <del>C</del> H <del>Q</del> L <del>V</del> IFAG <del>A</del> Q <del>T</del> KL <del>M</del> K <del>S</del> CKTK <del>F</del> K <del>R</del> TKID <del>Y</del> LM <del>Y</del> MY <del>T</del> IFV <del>V</del> LILL <del>S</del> AGLAIGHAY <del>W</del> E <del>A</del> QVGNSSW <del>Y</del> LYD	375
ATP8B2	R <del>N</del> T <del>E</del> W <del>Q</del> Y <del>G</del> L <del>V</del> IFAG <del>P</del> Q <del>T</del> KL <del>M</del> Q <del>S</del> CKTK <del>F</del> K <del>R</del> TSID <del>R</del> LM <del>T</del> LV <del>W</del> IFG <del>F</del> LVC <del>M</del> GVILAIGNA <del>I</del> WEHEVGMRFQ <del>V</del> YLP	344
ATP8B3	R <del>N</del> T <del>D</del> T <del>Q</del> Y <del>G</del> L <del>V</del> YIYAG <del>F</del> Q <del>T</del> KL <del>M</del> K <del>S</del> CKTK <del>F</del> K <del>R</del> TKID <del>Y</del> LM <del>Y</del> KL <del>V</del> V <del>V</del> IFIS <del>V</del> VLVCLVLAFG <del>F</del> GFSVKEFKDHHY <del>L</del> SG	499
ATP8B4	R <del>N</del> T <del>S</del> W <del>Q</del> Y <del>G</del> V <del>V</del> IFAG <del>P</del> Q <del>T</del> KL <del>M</del> Q <del>S</del> CKTK <del>F</del> K <del>R</del> TSID <del>R</del> LM <del>T</del> LV <del>W</del> IFG <del>F</del> LIC <del>L</del> GII <del>L</del> AIGNSIWESQ <del>T</del> G <del>D</del> Q <del>F</del> RT <del>L</del> FL	184
Consensus	nt c g v ag dtk m n g krt d n i	
H06H21.10a	WDDVVPSEQRGRQIALIAFLQFFSYIILLNTVPI <del>S</del> LYSV <del>E</del> IIRFIHSLWINYDTQMYYENGEKSV <del>P</del> AKA <del>H</del> T	394
ATP8B1	GEDDTPSYR..G.....FLIFWGYIIVLNTM <del>P</del> ISLYSV <del>E</del> IRLGQSHFINWDLQMYYEAKDT..PAKART	438
ATP8B2	WDEAVDSAFFSG.....FLSFWSYIILLNTVPI <del>S</del> LYSV <del>E</del> IRLGHSYFINWDKKMF <del>C</del> MKKRT..PAEART	409
ATP8B3	VHGSSVAAE <del>S</del> FFV <del>W</del> SFLILLSVTI <del>P</del> MSM <del>F</del> ILSEFIYLGNSV <del>F</del> IDWDVQMY <del>Y</del> KPQDVP <del>A</del> KARSTSLNDHLGQ <del>V</del> EY	574
ATP8B4	WNEGEKSSV <del>F</del> SG.....FLTFWSYIILLNTVPI <del>S</del> LYSV <del>E</del> IRLGHSYFINWDRKMY <del>Y</del> SRKA <del>I</del> ..PAVART	249
Consensus		

FIG.11B

H06H21_10a	TTLNEELGQVYFSDKTGTLTRNIMTFNKCTINGISYGDIDYHKGEVIEIENDKTKSLDFSWNSASEPTFKFFDK	469
ATP8B1	TTLNEQLQGIHYIFSDKTGTLTQNIMTFKKCCINGQIYGDRHDASQHNNKIEQ...VDFSWNITYADGKLAFYDH	513
ATP8B2	TTLNEELGQVEYIFSDKTGTLTQNIMVFVNKCSINCHSYGDFVDVLGHKAELGERPEPVDFSFNPLADKKFLWDP	484
ATP8B3	IFSCKTGTLTQNILTFNKCCIISGRVYCPDSEATTRPENPYL.....WNKFADGKLLFHNA	630
ATP8B4	TTLNEELGQIEYIFSDKTGTLTQNIMTFKRCSIINGRIYGEVHDDLQKTEITQEKEPVDFSVKSQADREFQFFDH	324

## Consensus

H06H21.10a	N <del>Z</del> VDA <del>T</del> KRQ <del>V</del> PEIDQ <del>F</del> WRL <del>Z</del> ALCH <del>T</del> WMPERDKQ...LVYQ.AQSPDEHAL <del>T</del> SAARNE <del>G</del> YV <del>F</del> RA <del>R</del> TPQSI <del>E</del>	538
ATP8B1	Y <del>Z</del> IEQISQKEPEVRQFF <del>Z</del> LA <del>V</del> CH <del>T</del> VMVDRTDG...QLNYQAA.SPDEGALVNAARNE <del>G</del> CFAL <del>R</del> ARTQNTI <del>S</del>	580
ATP8B2	S <del>Z</del> LEAVKIGDPH <del>T</del> HE.FFR <del>Z</del> SLCH <del>T</del> VMSEEKNE...GELYKACSPDEGALV <del>T</del> AAARNE <del>G</del> FV <del>R</del> SR <del>T</del> PKTI <del>V</del> H	554
ATP8B3	A <del>Z</del> LHLVRTNGDEAVREFW <del>R</del> LA <del>I</del> CH <del>T</del> VMVRESPRERPDQLLYQAA.SPDEGALV <del>T</del> AAARNE <del>G</del> YV <del>F</del> LS <del>R</del> TQDTV <del>I</del> M	704
ATP8B4	H <del>Z</del> MESIKMGDPKV <del>H</del> E.FLR <del>Z</del> ALCH <del>T</del> VMSEENSA...GELIYQVQSPDEGALV <del>T</del> AAARNE <del>G</del> IF <del>K</del> SP <del>T</del> PETI <del>E</del>	394

## Consensus

H06H21.10a	VMGNEETHELLAILDENINRKRMSVIVKGDCKIRLYCKGADMMIMQRIHPSTSQIMRTSTNT.....	601
ATP8B1	ELGTERTYNVAILDENSDRKRMSIIYRTPEGNKLYCKGADTVIYERLHRMNP TKQETQDALDI.....	645
ATP8B2	EMGTAITYQLAILDENINRKRMSVIVRNPECKIRLYCKGADTILLDRLHST...QELLNTTMD.....	619
ATP8B3	ELGGEERVYQVLAIMDENSTRKRMSVLVRKPECAICLYTKGADTVIFERLRRGAMEFATEEALAGQEEEEEAGEET	779
ATP8B4	ELGCTLVTYQLAFLDENINRKRMSVIVRNPECGQIKLYSKGADTILFEKLHPSN...EVLLSLTSD.....	459

## Consensus

Protein	Sequence	Position
H06H21.10a	HLADFANICRTTCLGCKDLDPAYFSWWD <del>SRVKKK</del> SAAMQDRESAVDALYEEI <del>EKDL</del>	658
ATP8B1	FANET...LRTTCLCCKEIEEKEFTET <del>INKKFM</del> AA <del>SVASTN</del> DEALDKVYEEI <del>EKDL</del>	698
ATP8B2	HLNEYAGEGLRTT <del>VLAK</del> DLDEEYEE <del>WAERLQ</del> ASLAQDSPEDRLASIEEY <del>ENNM</del>	673
ATP8B3	VRRNRLQVPGMAMYSEAFQET...LRTTCLAYREVAEDIYEDW <del>QQRHQE</del> ASLLLN <del>QAAQ</del> QQVY <del>NE</del> EQDL	850
ATP8B4	HLSEFAGEGLRTT <del>AIAR</del> DLDDKYFKE <del>WHKML</del> EDANAAATEE <del>EDER</del> IAGLYEEI <del>ERDL</del>	513

## Consensus

l r t l l y w a r y e e

**FIG. 11C**

H06H21.10a	IÉIGATAIÉDQKQDGPÉAIARÉSEANIKIHWLTGDKT.....	ÉTAIINIAYSÖRLÉTDEIKEI	716
ATP8B1	IÉIGATAIÉDQKQDGPÉITISKÉAKADIKIHWLTGDKK.....	ÉTAENIGFAÇELÉTEDTTIC	756
ATP8B2	MÉIGATAIÉDQKQDGPÉITIALÉTLANIKIHWLTGDKQ.....	ÉTAVNIIGYSÖKMÉTDDMTEV	731
ATP8B3	RÉIGATAIÉDRLQDGPÉITIKÉKKSNIKIHWLTGDKQSGQCGARRGAELVCFAE	ÉTAVNIIGFAÇELÉSENMLIL	925
ATP8B4	MÉIGATAVÉDQKQDGPÉITVTSÉSIANIKIHWLTGDKQ.....	ÉTAIINIIGYAÖNMÉTDDMNDV	571
Consensus	l gata ed lg gv e l ikiwvltgdk	eta ni c l	
H06H21.10a	VVDGQTDTEVEVQLKDRNTFEQILALPSLPGKPRIEIETIHEESEAISSARSMDRNIVTPDLKSAEMAEHES		791
ATP8B1	YGEDINSLHARMENQRNGVYAKFAPPVQESFFPPGGNRALIITGSWLNEILLEKTKRNKIL.....		821
ATP8B2	FIVTGHTVLEVREELRKAREKMDSSRSV.....	GNGFTYQDKLSSSKLTSVLEAVAGE.Y.....	786
ATP8B3	EEKEISRILETYWENSNNLLTRESLSQVKLALVINGDFLDKLLVSLRKEPRALAQNVNMEDAWQELGQSRDRFLY		1000
ATP8B4	FVIAGNNAVEVREELRKAKQNLFGQNRNF.....	SNGHVCEKKQQLDLSIVEETITGDY.....	627
Consensus			
H06H21.10a	GGVALVINGDSLAFALGPRLERTFLEV.....	ÁCMENAVIICCRVTPQLQKAQVVDLÁVRNKKAVIÉSL	853
ATP8B1	...KLKFPRTTEEERRMRTQSKRRLEAKKEQRQKN..FVDLÁCEESAVIICCRVTPKQKAMVVDLÁVRKKAIAIÉAI		891
ATP8B2	...ALVINGHSLAHALEADMELEFLET.....	ÁCAÇKAVIICCRVTPQLQKAQVVDLÁVRKKAIAIÉAI	845
ATP8B3	ARRLSLLCRREFGLPAAPPAQDSRARRSSEVLQERAFVDLÁSKÇQAVIICCRVTPKQKALIVALEÁVRKYHQVWÉAI		1075
ATP8B4	...ALVINGHSLAHALESDVKNDLLEL.....	ÁCMÇKTVIICCRVTPQLQKAQVVDLÁVRKKAIAIÉAI	686
Consensus		a c viccervtp qka v lvk t l i	
H06H21.10a	QÇÇANDVSMKKTÁHICVÇGISÇQÇÇMÇQAVLÁSDYSIGÇÇKÇYÇERLLLVHÇRWSYIRMAKÇLRÇYÇYKÇNFÁFTLINF		928
ATP8B1	QÇÇANDVNMKKTÁHICVÇGISÇQÇÇMÇQAVMSÇDYSFAÇRYÇQRLLLVHÇRWSYIRMCKÇLRÇYÇYKÇNFÁFTLVHF		966
ATP8B2	QÇÇANDVSMKKTÁHICVÇGISÇQÇÇIQAVLÁSDYSFSÇQKFÇQRLLLVHÇRWSYLRMCKÇLCYÇYKÇNFÁFTMVHF		920
ATP8B3	QÇÇANDINMKKTÁDVÇVÇLAGÇQÇÇMÇQAVQNÇDÇFVLÇQÇCFÇQRLLLVHÇRWSYVRICKÇLRÇYÇYKÇSMÇSMMVQV		1150
ATP8B4	QÇÇANDVSMKKTSAHICVÇGISÇQÇÇLÇQAVLÁSDYSFAÇRYÇQRLLLVHÇRWSYFIRMCKÇLCYÇYKÇNFÁFTLVHF		761
Consensus	gdgand mik a gvg ggeg qav sd qf l rlllvhgrwsy r kfl yfyk a		

FIG.11D

H06H21.10a	<del>WYSFFCQYSAQ</del> TVFDAVL IACY <del>WLF</del> FTAL <del>PV</del> AMGSL <del>DQD</del> DDHYSLRY <del>P</del> KEL <del>PL</del> PC <del>Q</del> FNLF <del>FM</del> MRIFIYSVLHGM	1003
ATP8B1	<del>WYSFFNQYSAQ</del> TAYEDWFI <del>TL</del> Y <del>W</del> VL <del>Y</del> TS <del>SL</del> PV <del>EL</del> MG <del>LL</del> DQD <del>Y</del> SDKL <del>SL</del> RF <del>PG</del> EL <del>IV</del> GG <del>RD</del> LL <del>FN</del> YKRFFVSLLHGV	1041
ATP8B2	<del>WFGFFCQYSAQ</del> TVYDQYFI <del>TL</del> Y <del>W</del> IV <del>Y</del> TS <del>SL</del> PV <del>EL</del> AMG <del>V</del> FDQ <del>Y</del> PEQR <del>SM</del> EY <del>P</del> KEL <del>PE</del> Q <del>LL</del> NLL <del>FN</del> KREFFICIAQGI	995
ATP8B3	<del>W</del> FACYN <del>Q</del> FTG <del>Q</del> PL YEGWFLALF <del>LL</del> YST <del>SL</del> PV <del>EL</del> Y <del>Q</del> GLFEQ <del>Y</del> SAEQ <del>SL</del> EK <del>P</del> EL <del>VV</del> GG <del>Q</del> DEL <del>FN</del> YWV <del>F</del> VQAIAGV	1225
ATP8B4	<del>WFGFFCQYSAQ</del> TVYDQWFI <del>TL</del> Y <del>W</del> IV <del>Y</del> TS <del>SL</del> PV <del>EL</del> AMG <del>I</del> FDQ <del>Y</del> SDQN <del>SV</del> DCPQ <del>Y</del> K <del>P</del> Q <del>LL</del> NLL <del>FN</del> KRKFFICVLHG	836
Consensus	w g q n l p v l g q d v s p l y g q f n f g	
H06H21.10a	F <del>S</del> L <del>V</del> I <del>FF</del> IPYCAFYNAAAASGKDLD <del>Y</del> SAL <del>AF</del> TTFTALV..VVTGQIAFDTSYMTAISHFVIWGSLLVFLVC	1076
ATP8B1	L <del>T</del> S <del>M</del> I <del>L</del> FFIPLGAYLQTVGDGEAPSDYQSF <del>AV</del> TIASALV..ITVNGQICLDTSYMTFVNAFSIFGSIALYFGIM	1114
ATP8B2	Y <del>T</del> S <del>V</del> L <del>M</del> FFIPYGVFADATRDDGTQLA <del>Y</del> QSF <del>AV</del> TVATSLV..I <del>V</del> SV <del>V</del> QICLDTGYMTA <del>I</del> NHFFIWGS <del>L</del> AVYFAIL	1068
ATP8B3	T <del>T</del> S <del>L</del> V <del>N</del> FFMTLWISRD <del>T</del> AGPASF..S <del>Q</del> HQSF <del>AV</del> VVALSCLLSITMEVGKVLTPSPWTW <del>P</del> MEASSPGDPCFGGIA	1298
ATP8B4	Y <del>T</del> S <del>L</del> V <del>L</del> FFIPYCAFYNVAGEDCQ <del>H</del> IA <del>Y</del> QSF <del>AV</del> TMATSLV..I <del>V</del> SV <del>V</del> QIALDTSYMTFINHVFIWGS <del>I</del> AIYFSIL	909
Consensus	s f f d a	
H06H21.10a	FLLYEWL <del>P</del> VS <del>W</del> I <del>V</del> K <del>T</del> SSSISYGVAFRTMT <del>P</del> HF <del>W</del> FSILM <del>V</del> SV <del>V</del> LLLPV <del>M</del> LNR <del>F</del> FWL <del>D</del> THPSFADRLRIRK <del>K</del> MGKK	1151
ATP8B1	FDFHSAGI <del>H</del> VLFP <del>S</del> AFQFTGTASNALR <del>P</del> QYI <del>W</del> L <del>T</del> IILTV..AVCLLPV <del>V</del> AIR <del>F</del> LSMTIWPSESDKI <del>Q</del> KH...RKR	1184
ATP8B2	FAMHSNCLFDM <del>F</del> PNQFRFV <del>G</del> NAQNTLAQPT <del>V</del> WL <del>T</del> I <del>V</del> LT..VVCIMPV <del>V</del> AFR <del>F</del> LRLNLKPDLS <del>D</del> TVRYTQLVRKK	1141
ATP8B3	RCPSWTPGAGVLVQAPLGP <del>G</del> FTPPLPVQVILIIKYWTALCVATILLSLGFYAIM <del>T</del> TTTTSQSWLFRVSP <del>T</del> TFPFL.	1372
ATP8B4	FTMHSNGIFGIFPNQFPFVGNARHSLTQKCIWL <del>V</del> ILLTT..VASVMPV <del>V</del> AFR <del>F</del> LKV <del>D</del> LYPTLSQ <del>I</del> RRWQKAQKK	982
Consensus		
H06H21.10a	PSAKDDKKTAFKRTAAT...RRSVRGLRSGYAFSHSQGF <del>G</del> ELILKGKLFKNVENLRGKNNSNAKIHPTSDDLQP	1223
ATP8B1	LKAEQWQRRQVFRRGVSTRRSAYAFSHQRCYADLISSGRSI.....RKKRSP	1233
ATP8B2	QKAQHRCMRRVGR <del>T</del> GS...RRSGYAFSHQEGF <del>G</del> ELIMSGKNMRLSSLALSSF <del>T</del> TRSS...SWIESLRRK <del>K</del> SDS	1209
ATP8B3	.....YADLSVMSSPSILLVLLSVSINTFPVLARVIFPALKELRAK	1415
ATP8B4	ARPPSSRRPRTRRSS...RRSGYAFAHQEGY <del>G</del> ELITSGKNMRAKNPPPTSGLEKTHYNSTSWIENLCKKTTDT	1053
Consensus		

FIG.11E

H06H21.10a	MLISSVPDDSQGASSINAMHLPMGTRPQNVPHTLNVNTDDWSQSSDFRPAYAKEPSPLQGTVIRGDCGRSHRNHVY	1298
ATP8B1	LDAIVADGTAEYRRTGDS	1251
ATP8B2	ASSPSGGADKPLKG	1223
ATP8B3	EKKVEEGPSEEIFTMEPLPHVHRESRARRSSYAFSHREGYANLITQGTILRRGPGVSSDIASESLDPSDEEAASS	1490
ATP8B4	VSSFSQDKTVKL	1065
Consensus		
H06H21.10a	SRETQVEEQPDVITRL	1314
ATP8B1		1251
ATP8B2		1223
ATP8B3	PKESQ	1495
ATP8B4		1065
Consensus		

FIG. 11F